

SRNT



Entrez

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Protein

Genome

Structure

OMIM

PMC

Journals

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About Entrez

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- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.

Entrez PubMed

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#55 Search #54 AND fusion	11:36:22	<u>8</u>
#54 Related Articles for PubMed (Select 8322511)	11:33:59	<u>157</u>
#52 Search pir2 hsp150	10:53:27	<u>6</u>
#45 Search #42 AND yeast	10:46:55	<u>26</u>
#42 Related Articles for PubMed (Select 9023548)	10:40:07	<u>109</u>
#40 Search l-selectin yeast	10:39:38	<u>17</u>
#39 Search l-selectin	10:39:26	<u>2608</u>
#38 Search matilla glycobiology	10:39:13	<u>0</u>
#37 Search matilla targeting	10:39:03	<u>0</u>
#36 Search matilla fusion	10:38:45	<u>0</u>
#35 Search matilla lewis	10:38:31	<u>0</u>
#34 Search matilla yeast	10:38:08	<u>3</u>
#9 Related Articles for PubMed (Select 12626410)	08:50:33	<u>104</u>
#32 Search #30 AND pir	08:45:49	<u>3</u>
#30 Related Articles for PubMed (Select 12766345)	08:45:18	<u>95</u>
#28 Search zueco fusion	08:40:51	<u>5</u>
#27 Search jaafar fusion	08:40:40	<u>1</u>
#26 Search moukadiri fusion	08:40:29	<u>1</u>
#25 Search pir1 fusion	08:13:49	<u>4</u>
#24 Search jigami and pir	08:09:50	<u>2</u>
#23 Search shimma and pir	08:09:39	<u>2</u>
#22 Search yoh-ichi and pir	08:09:14	<u>0</u>
#21 Search ohba and pir	08:08:48	<u>2</u>
#20 Search abe and pir	08:08:36	<u>3</u>
#18 Search #17 AND pir	08:07:11	<u>9</u>
#17 Related Articles for PubMed (Select 10438739)	08:06:53	<u>103</u>
#16 Search #9 AND pir	08:06:39	<u>6</u>
#7 Search #6 and pir	08:00:37	<u>12</u>
#6 Related Articles for PubMed (Select 14734022)	08:00:08	<u>94</u>
#2 Search #1 AND fusion	07:59:42	<u>46</u>
#1 Search pir	07:53:08	<u>976</u>

(FILE 'HOME' ENTERED AT 13:10:57 ON 11 FEB 2004)

FILE 'REGISTRY' ENTERED AT 13:11:39 ON 11 FEB 2004

L1 13 S PIR1

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
13:12:00 ON 11 FEB 2004

L2 2 S L1 AND FUSION

L3 6 S L1 AND (CELL (W) WALL)

L4 5 DUP REM L3 (1 DUPLICATE REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:14:26 ON 11 FEB 2004

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
13:19:09 ON 11 FEB 2004

L5 93 S (PIR1? OR PIR2? OR PIR3? OR PIR4?) AND (YEAST OR CEREVISIAE)

L6 60 S L5 AND (FUSION OR (CELL (W) WALL))

L7 19 DUP REM L6 (41 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:21:23 ON 11 FEB 2004

FILE 'CAPLUS' ENTERED AT 13:23:55 ON 11 FEB 2004

E ABE HIR/AU 25

L8 3 S (E19 OR E20) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR!)

E SHIMMA YOH/AU 25

L9 3 S (E4 OR E5 OR E6) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR

E JIGAMI YO/AU 25

L10 3 S (E4 OR E5) AND (PIR1? OR PIR2? OR PIR3? OR PIR4? OR PIR!)

=>

RESULT 1

YSCPIR1P

LOCUS YSCPIR1P 1400 bp DNA linear PLN 03-FEB-1999

DEFINITION S. cerevisiae Pirlp gene.

ACCESSION D13740

VERSION D13740.1 GI:218456

KEYWORDS Pirlp.

SOURCE Saccharomyces cerevisiae (baker's yeast)

ORGANISM Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 1400)

AUTHORS Toh-e,A., Yasunaga,S., Nisogi,H., Tanaka,K., Oguchi,T. and
Matsui,Y.TITLE Three yeast genes, PIR1, PIR2 and PIR3, containing internal tandem
repeats, are related to each other, and PIR1 and PIR2 are required
for tolerance to heat shock

JOURNAL Yeast 9 (5), 481-494 (1993)

MEDLINE 93311116

PUBMED 8322511

REFERENCE 2 (bases 1 to 1400)

AUTHORS Toh-e,A.

TITLE Direct Submission

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Fax:03-5684-9420)

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Fax: 03-5684-9420.

FEATURES Location/Qualifiers

source

1. .1400

/organism="Saccharomyces cerevisiae"

/mol_type="genomic DNA"

/db_xref="taxon:4932"

gene

139. .1164

/gene="PIR1"

CDS

139. .1164

/gene="PIR1"

/codon_start=1

/product="Pirlp"

/protein_id="BAA02885.1"

/db_xref="GI:218457"

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A A V S Q I G D G Q I Q A T T K T T S A K T T A A A V S Q I G D G Q I Q A T T K T K A A A V S Q I G D G Q I Q A T T
K T T A A A V S Q I G D G Q I Q A T T K T T A A A V S Q I G D G Q I Q A T T N T T V A P V S Q I T D G Q I Q A T T L
T S A T I I P S P A P A P I T N G T D P V T A E T C K S S G T L E M N L K G G I L T D G K G R I G S I V A N R Q F Q
F D G P P P Q A G A I Y A A G W S I T P E G N L A I G D Q D T F Y Q C L S G N F Y N L Y D E H I G T Q C N A V H L Q
A I D L L N C"

BASE COUNT 415 a 350 c 221 g 414 t

ORIGIN

Alignment Scores:

Pred. No.:	6.15e-92	Length:	1400
Score:	1708.00	Matches:	341
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-989-975-1 (1-341) x YSCPIR1P (1-1400)

Qy	1	MetGlnTyrLysLysSerLeuValAlaSerAlaLeuValAlaThrSerLeuAlaAlaTyr	20
Db	139	ATGCAATACAAAAAATCATTAGTTGCCTCCGCCTTAGTTGCTACATCTTTAGCTGCCTAT	198
Qy	21	AlaProLysAspProTrpSerThrLeuThrProSerAlaThrTyrLysGlyGlyIleThr	40
Db	199	GCTCCAAAGGACCCGTGGTCCACTTTAACTCCATCAGCTACTTACAAGGGTGGTATAACT	258
Qy	41	AspTyrSerSerThrPheGlyIleAlaValGluProIleAlaThrThrAlaSerSerLys	60
Db	259	GATTACTCTTCTACTTTTCGGTATTGCTGTTGAACCAATTGCCACTACTGCTTCCTCCAAG	318
Qy	61	AlaLysArgAlaAlaAlaIleSerGlnIleGlyAspGlyGlnIleGlnAlaThrThrLys	80
Db	319	GCTAAGAGAGCCGCTGCTATCTCTCAAATTGGTGACGGTCAAATCCAAGCCACTACCAAA	378
Qy	81	ThrThrAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThrThrLysThr	100
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Qy	101	LysAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThrThrLysThrThr	120
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Qy	121	SerAlaLysThrThrAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThr	140
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Qy	141	ThrLysThrLysAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThrThr	160
Db	559	ACTAAAACCAAAGCTGCTGCTGTCTCTCAAATTGGTGACGGTCAAATCCAAGCCACTACC	618
Qy	161	LysThrThrAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThrThrLys	180
Db	619	AAAACAACTGCTGCAGCTGTCTCTCAAATTGGTGACGGTCAAATCCAAGCCACTACTAAA	678
Qy	181	ThrThrAlaAlaAlaValSerGlnIleGlyAspGlyGlnIleGlnAlaThrThrAsnThr	200
Db	679	ACCACTGCTGCTGCTGTTTCTCAAATTGGTGACGGTCAAATCCAAGCCACCACCAATACT	738
Qy	201	ThrValAlaProValSerGlnIleThrAspGlyGlnIleGlnAlaThrThrLeuThrSer	220
Db	739	ACTGTTGCTCCAGTCTCCCAAATCACTGATGGCCAAATCCAAGCCACAAC'TTTAACTTCT	798
Qy	221	AlaThrIleIleProSerProAlaProAlaProIleThrAsnGlyThrAspProValThr	240

Db	799		GCAACCATTATACCATCTCCAGCTCCAGCTCCAATTACTAATGGCACTGACCCAGTAACT	858
Qy	241		AlaGluThrCysLysSerSerGlyThrLeuGluMetAsnLeuLysGlyGlyIleLeuThr	260
Db	859		GCTGAAACATGTAAAAGCAGTGGCACTTTAGAAATGAACTTAAAGGGTGGTATCCTGACT	918
Qy	261		AspGlyLysGlyArgIleGlySerIleValAlaAsnArgGlnPheGlnPheAspGlyPro	280
Db	919		GACGGTAAAGGTAGAATTGGTTCTATCGTTGCCAACAGACAATTCCAATTCGATGGTCCT	978
Qy	281		ProProGlnAlaGlyAlaIleTyrAlaAlaGlyTrpSerIleThrProGluGlyAsnLeu	300
Db	979		CCACCACAAGCTGGTGCTATCTATGCTGCTGGTTGGTCCATCACCCAGAAGGTAACCTTG	1038
Qy	301		AlaIleGlyAspGlnAspThrPheTyrGlnCysLeuSerGlyAsnPheTyrAsnLeuTyr	320
Db	1039		GCCATCGGTGACCAGGATACTTTTTACCAATGTTTGTGAGGAACTTCTACAACCTTATAC	1098
Qy	321		AspGluHisIleGlyThrGlnCysAsnAlaValHisLeuGlnAlaIleAspLeuLeuAsn	340
Db	1099		GATGAGCACATTGGAACCTCAATGTAATGCAGTCCACCTACAAGCTATCGATTTGCTCAAC	1158
Qy	341		Cys 341	
Db	1159		TGT 1161	